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=> s avr1 (p) co39

L1 12 AVR1 (P) CO39

=> s co39 (p) avirulen?

L2 13 CO39 (P) AVIRULEN?

=> dup rem l1

PROCESSING COMPLETED FOR L1
L3 6 DUP REM L1 (6 DUPLICATES REMOVED)

=> dup rem l3

PROCESSING COMPLETED FOR L3
L4 6 DUP REM L3 (0 DUPLICATES REMOVED)

=> d l3 ti 1-6

L3 ANSWER 1 OF 6 CAPLUS COPYRIGHT 2000 ACS DUPLICATE 1
TI Mapping of avirulence genes in the rice blast fungus, Magnaporthe grisea, with RFLP and RAPD markers

L3 ANSWER 2 OF 6 BIOSIS COPYRIGHT 2000 BIOSIS
TI Molecular and cytological studies of early stages of infection caused by strains of Pyricularia grisea transformed with an avirulence gene, **AVR1-CO39**.

L3 ANSWER 3 OF 6 CAPLUS COPYRIGHT 2000 ACS

its use in improving plant resistance to rice blast

- L3 ANSWER 4 OF 6 AGRICOLA DUPLICATE 2
TI Chromosome walking to the **AVR1-CO39** avirulence gene of
Magnaporthe grisea: discrepancy between the physical and genetic maps.
- L3 ANSWER 5 OF 6 BIOSIS COPYRIGHT 2000 BIOSIS
TI An effort to clone a rice blast resistance gene corresponding to
avirulence gene AVR1-C039 of Magnaporthe grisea.
- L3 ANSWER 6 OF 6 AGRICOLA DUPLICATE 3
TI Magnaporthe grisea genes for pathogenicity and virulence identified
through a series of backcrosses.

=> d 14 ti 1-6

- L4 ANSWER 1 OF 6 CAPLUS COPYRIGHT 2000 ACS
TI Mapping of avirulence genes in the rice blast fungus, Magnaporthe grisea,
with RFLP and RAPD markers
- L4 ANSWER 2 OF 6 BIOSIS COPYRIGHT 2000 BIOSIS
TI Molecular and cytological studies of early stages of infection caused by
strains of Pyricularia grisea transformed with an avirulence gene,
AVR1-CO39.
- L4 ANSWER 3 OF 6 CAPLUS COPYRIGHT 2000 ACS
TI A cultivar specificity gene of the rice pathogen Magnaporthe grisea and
its use in improving plant resistance to rice blast
- L4 ANSWER 4 OF 6 AGRICOLA
TI Chromosome walking to the **AVR1-CO39** avirulence gene of
Magnaporthe grisea: discrepancy between the physical and genetic maps.
- L4 ANSWER 5 OF 6 BIOSIS COPYRIGHT 2000 BIOSIS
TI An effort to clone a rice blast resistance gene corresponding to
avirulence gene AVR1-C039 of Magnaporthe grisea.
- L4 ANSWER 6 OF 6 AGRICOLA
TI Magnaporthe grisea genes for pathogenicity and virulence identified
through a series of backcrosses.

=> d ibib ab 1-6

L4 ANSWER 1 OF 6 CAPLUS COPYRIGHT 2000 ACS
ACCESSION NUMBER: 2000:71594 CAPLUS
DOCUMENT NUMBER: 133:1242
TITLE: Mapping of avirulence genes in the rice blast fungus,
Magnaporthe grisea, with RFLP and RAPD markers
AUTHOR(S): Doh, Waly; Tharreau, Didier; Notteghem, Jean Loup;
Orbach, Marc; Lebrun, Marc-Henri
CORPORATE SOURCE: Genetique Moleculaire des Champignons
Phytopathogenes,
Institut de Genetique et Microbiologie, CNRS-URA
2255,
Universite Paris-Sud, Orsay, 91405, Fr.
SOURCE: Mol. Plant-Microbe Interact. (2000), 13(2), 217-227
CODEN: MPMIEL; ISSN: 0894-0282
PUBLISHER: APS Press
DOCUMENT TYPE: Journal
LANGUAGE: English

AVR1-CO39

AVR1-MedNol, and **AVR1**-Ku86, were identified in a cross involving isolates Guy11 and 2/0/3 of the rice blast fungus, *Magnaporthe grisea*. Using 76 random progeny, the authors constructed a partial genetic map with restriction fragment length polymorphism (RFLP) markers revealed by probes such as the repeated sequences MGL/MGR583 and Pot3/MGR586, cosmids from the *M. grisea* genetic map, and a telomere sequence oligonucleotide. Avirulence genes **AVR1**-MedNol and **AVR1**-Ku86 were closely linked to telomere RFLPs such as marker TelG (6 cM from **AVR1**-MedNol) and TelF (4.5 cM from **AVR1**-Ku86). Avirulence gene **AVR1**-Irat7 was linked to a cosmid RFLP located on chromosome 1 and mapped at 20 cM from the avirulence gene **AVR1**-CO39. Using bulked segregant anal., the authors identified 11 random amplified polymorphic DNA (RAPD) markers closely linked (0 to 10 cM) to the avirulence genes segregating in this cross. Most of these RAPD markers corresponded to junction fragments between known or new transposons and a single-copy sequence. Such junctions or the whole sequences of single-copy RAPD markers were frequently absent in one parental isolate. Single-copy sequences from RAPD markers tightly linked to avirulence genes will be used for positional cloning.

REFERENCE COUNT: 66

REFERENCE(S): (1) Arnau, J; Curr Genet 1994, V25, P438 CAPLUS
(2) Bhattacharyya, M; Plant Mol Biol 1997, V34, P255 CAPLUS
(3) Biessmann, H; Advances in Genetics 1992, V30,

P185

CAPLUS
(5) Daboussi, M; Curr Genet 1989, V15, P453 CAPLUS
(6) Daboussi, M; Genetica 1994, V93, P49 CAPLUS
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L4 ANSWER 2 OF 6 BIOSIS COPYRIGHT 2000 BIOSIS

ACCESSION NUMBER: 2000:326561 BIOSIS

DOCUMENT NUMBER: PREV200000326561

TITLE: Molecular and cytological studies of early stages of infection caused by strains of *Pyricularia grisea* transformed with an avirulence gene, **AVR1**-CO39.

AUTHOR(S): Nalim, F. A. (1); Farman, M. L. (1)

CORPORATE SOURCE: (1) Dept. of Plant Pathology, University of Kentucky, Lexington, KY, 40546 USA

SOURCE: Phytopathology, (June, 2000) Vol. 90, No. 6 Supplement, pp.

S55. print.

Meeting Info.: Annual Meeting of the American Phytopathological Society New Orleans, Louisiana, USA August 12-16, 2000 American Phytopathological Society . ISSN: 0031-949X.

DOCUMENT TYPE: Conference

LANGUAGE: English

SUMMARY LANGUAGE: English

L4 ANSWER 3 OF 6 CAPLUS COPYRIGHT 2000 ACS

ACCESSION NUMBER: 1999:566190 CAPLUS

DOCUMENT NUMBER: 131:182483

TITLE: A cultivar specificity gene of the rice pathogen *Magnaporthe grisea* and its use in improving plant resistance to rice blast

INVENTOR(S): Leong, Sally A.; Farman, Mark L.

PATENT ASSIGNEE(S): Wisconsin Alumni Research Foundation, USA

SOURCE: PCT Int. Appl., 45 pp.

CODEN: PIXXD2

DOCUMENT TYPE: Patent

LANGUAGE: English

FAMILY ACC. NUM. COUNT: 1

REMARKS: INFORMATION

| PATENT NO. | KIND | DATE | APPLICATION NO. | DATE |
|---|------|--|-----------------|----------|
| WO 9943824 | A1 | 19990902 | WO 1999-US4047 | 19990225 |
| <p>W: AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM</p> <p>RW: GH, GM, KE, LS, MW, SD, SL, SZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG</p> | | | | |
| AU 9933105 | A1 | 19990915 | AU 1999-33105 | 19990225 |
| PRIORITY APPLN. INFO.: | | | US 1998-75925 | 19980225 |
| | | | WO 1999-US4047 | 19990225 |
| <p>AB A novel avirulence gene, AVR1-CO39, from the rice blast pathogen <i>Magnaporthe grisea</i> that confers cultivar-specific avirulence to strains of <i>M. grisea</i> that carry it is described. The gene may be used in the development of rice strains with improved resistance to rice blast. Map-based methods were used to clone the gene. Identity of the gene was confirmed by its conversion of a strain of <i>M. grisea</i> normally virulent to CO39 rice to avirulence. The gene contained several open reading frames encoding small polypeptides and two of them were shown to be involved in the avirulence process by mutation. The gene, or sequences cross-hybridizing with it, were not found in strains infecting rice, <i>Digitaria</i>, and wheat. The gene was expressed in <i>Escherichia coli</i> and exts. sprayed on rice plants. Sprayed plants showed greater resistance to subsequent <i>M. grisea</i> infection than did control plants.</p> | | | | |
| REFERENCE COUNT: | | 10 | | |
| REFERENCE(S): | | <p>(1) Cornell Res Foundation Inc; WO 9639802 A 1996</p> <p>(2) Farman, M; GENETICS 1998, V150(3), P1049 CAPLUS</p> <p>(6) Smith, J; THEOR APPL GENET 1994, V88, P901 CAPLUS</p> <p>(7) Sweigard, J; PLANT CELL 1995, V7, P1221 CAPLUS</p> <p>(10) Valent, B; GENETICS 1991, V127, P87 MEDLINE</p> <p>ALL CITATIONS AVAILABLE IN THE RE FORMAT</p> | | |
| L4 ANSWER 4 OF 6 AGRICOLA | | | | |
| ACCESSION NUMBER: | | 1999:12362 AGRICOLA | | |
| DOCUMENT NUMBER: | | IND21966917 | | |
| TITLE: | | Chromosome walking to the AVR1-CO39 avirulence gene of <i>Magnaporthe grisea</i> : discrepancy between the physical and genetic maps. | | |
| AUTHOR(S): | | Farman, M.L.; Leong, S.A. | | |
| CORPORATE SOURCE: | | University of Kentucky, Lexington. | | |
| AVAILABILITY: | | DNAL (442.8 G28) | | |
| SOURCE: | | Genetics, Nov 1998. Vol. 150, No. 3. p. 1049-1058 | | |
| | | Publisher: Bethesda, Md. : Genetics Society of America. | | |
| | | CODEN: GENTAE; ISSN: 0016-6731 | | |
| NOTE: | | Includes references | | |
| PUB. COUNTRY: | | Maryland; United States | | |
| DOCUMENT TYPE: | | Article | | |
| FILE SEGMENT: | | U.S. Imprints not USDA, Experiment or Extension | | |
| LANGUAGE: | | English | | |
| L4 ANSWER 5 OF 6 BIOSIS COPYRIGHT 2000 BIOSIS | | | | |
| ACCESSION NUMBER: | | 1998:462768 BIOSIS | | |
| DOCUMENT NUMBER: | | PREV199800462768 | | |
| TITLE: | | An effort to clone a rice blast resistance gene corresponding to avirulence gene AVR1-CO39 of <i>Magnaporthe</i> | | |

AUTHOR(S): Chauhan, R. S. (1); Farman, M. L.; Ronald, P.; Leong, S. A.
CORPORATE SOURCE: (1) Univ. Wisconsin, Madison, WI 53706 USA
SOURCE: Phytopathology, (Sept., 1998) Vol. 88, No. 9 SUPPL., pp. S15.
Meeting Info.: Annual Meeting of the American
Phytopathological Society Las Vegas, Nevada, USA November
8-12, 1998 American Phytopathological Society
. ISSN: 0031-949X.
DOCUMENT TYPE: Conference
LANGUAGE: English

L4 ANSWER 6 OF 6 AGRICOLA

ACCESSION NUMBER: 91:31052 AGRICOLA
DOCUMENT NUMBER: IND91013420
TITLE: Magnaporthe grisea genes for pathogenicity and
virulence identified through a series of backcrosses.
AUTHOR(S): Valent, B.; Farrall, L.; Chumley, F.G.
CORPORATE SOURCE: The Du Pont Company, Wilmington, Delaware
AVAILABILITY: DNAL (442.8 G28)
SOURCE: Genetics, Jan 1991. Vol. 127, No. 1. p. 87-101 ill
Publisher: Baltimore, Md. : Genetics Society of
America.
CODEN: GENTAE; ISSN: 0016-6731
NOTE: Includes references.
DOCUMENT TYPE: Article
FILE SEGMENT: U.S. Imprints not USDA, Experiment or Extension
LANGUAGE: English

AB We have identified genes for pathogenicity toward rice (*Oryza sativa*) and
genes for virulence toward specific rice cultivars in the plant
pathogenic

fungus *Magnaporthe grisea*. A genetic cross was conducted between the
weeping lovegrass (*Eragrostis curvula*) pathogen 4091-5-8, a highly
fertile, hermaphroditic laboratory strain, and the rice pathogen O-135, a
poorly fertile, female-sterile field isolate that infects weeping
lovegrass as well as rice. A six-generation backcrossing scheme was then
undertaken with the rice pathogen as the recurrent parent. One goal of
these crosses was to generate rice pathogenic progeny with the high
fertility characteristic of strain 4091-5-8, which would permit rigorous
genetic analysis of rice pathogens. Therefore, progeny strains to be used
as parents for backcross generations were chosen only on the basis of
fertility. The ratios of pathogenic to nonpathogenic (and virulent to
avirulent) progeny through the backcross generations suggested that the
starting parent strains differ in two types of genes that control the
ability to infect rice. First, they differ by polygenic factors that
determine the extent of lesion development achieved by those progeny that
infect rice. These genes do not appear to play a role in infection of
weeping lovegrass because both parents and all progeny infect weeping
lovegrass. Second, the parents differ by simple Mendelian determinants,
"avirulence genes," that govern virulence toward specific rice cultivars
in all-or-none fashion. Several crosses confirm the segregation of three
unlinked avirulence genes, **Avr1-CO39**, **Avr1**
-M201 and **Avr1-YAMO**, alleles of which determine avirulence on
rice cultivars **CO39**, M201, and Yashiro-mochi, respectively.
Interestingly, avirulence alleles of **Avr1-CO39**,
Avr1-M201 and **Avr1-YAMO** were inherited from the parent
strain 4091-5-8, which is a nonpathogen of rice. Middle repetitive DNA
sequences ("MGR sequences"), present in approximately 40-50 copies in the
genome of the rice pathogen parent, and in very low copy, number in the
genome of the nonpathogen of rice, were used as physical markers to
monitor restoration of the rice pathogen genetic background during
introgression of fertility. The introgression of highest levels of
fertility into the most successful rice pathogen progeny was incomplete

by

genes for fertility and genes for rice pathogenicity. One chromosomal DNA segment with MGR sequence homology appeared to be linked to the gene **Avr1-CO39**. Finally, many of the crosses described in this paper exhibited a characteristic common to many crosses involving *M. grisea* rice pathogen field isolates. That is, pigment-defective mutants frequently appeared among the progeny.